

FIG. 1

2/17

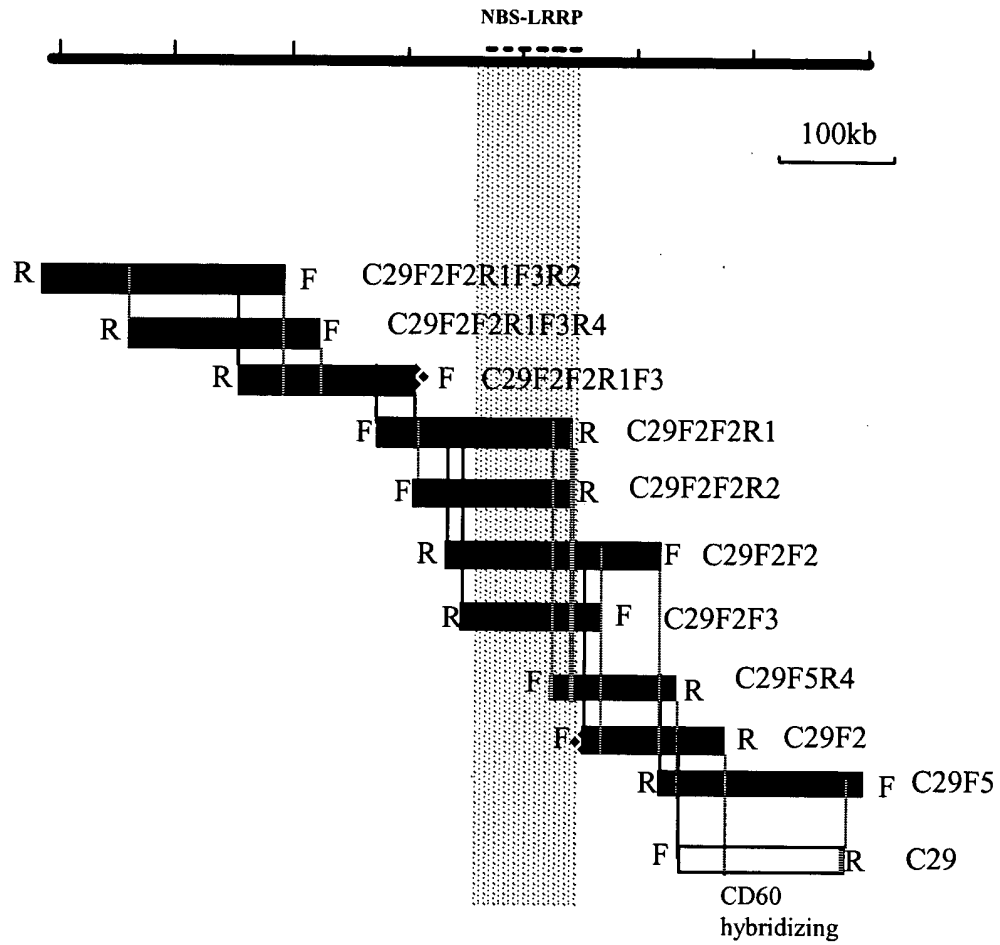


FIG. 2

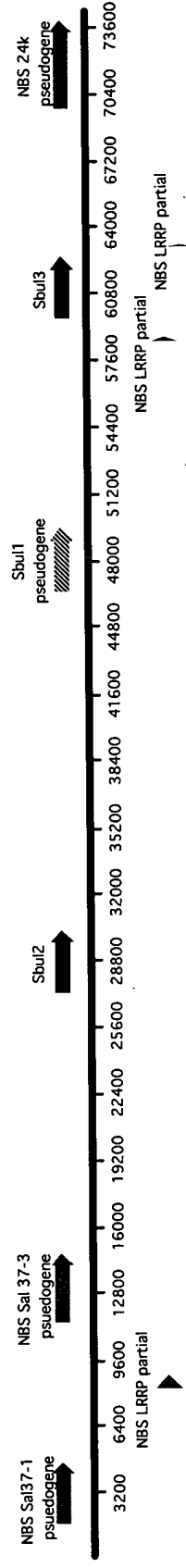
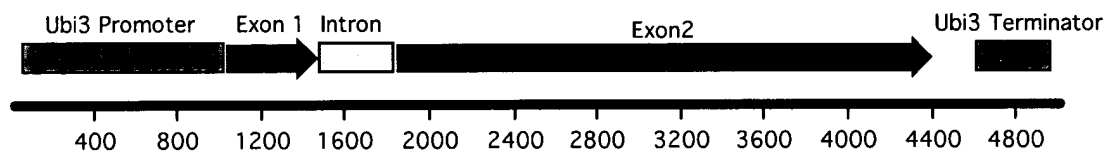


FIG. 3

4/17

Sbul1 Genomic Transgene



Sbul1 cDNA Transgene

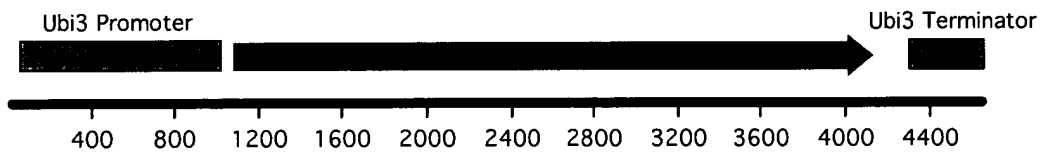


FIG. 4

5/17

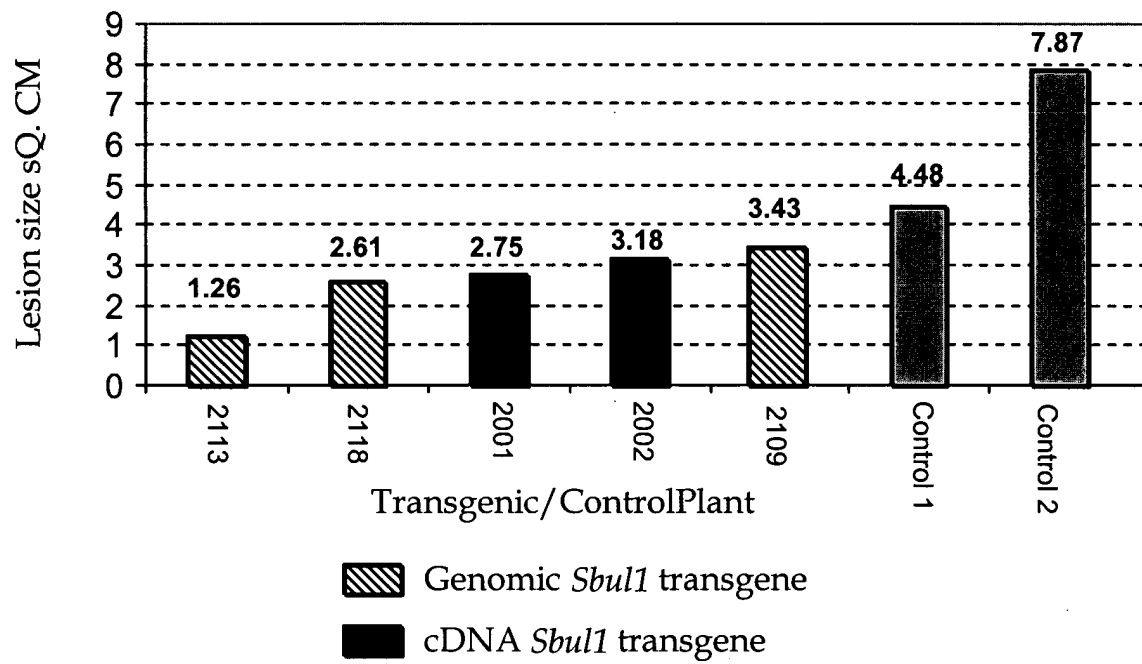


FIG. 5

6/17

**Alignment of *Sbul1* (SEQ ID NO:4) and *Sbul2* (SEQ ID NO:6)
deduced Amino Acid sequences**

```

Sbul1:    MAEAFQVLLDNLTCFIQGELGLILGFKDEFEKLQSTFTTIQAVLEDAQKKQLKDKAIE
Sbul2:    MAEAFQVLLDNLTCFIQGEVGLILGFKDEFEKLQSTFTTIQAVLEDAQKKQLKDKAIE

Sbul1:    WLQKLNAAYEADDILDECKTEAPIRQKKNKYGCYHPNVITFRHKIGKRMKKIMEKLDVI
Sbul2:    WLQKLNAAYEADDILDECKTEAPIRQKKNKYGCYHPNVIAFRHKIGKRMKKIMEKLDVI

Sbul1:    AAERIKFHLDER TIERQVATRQTG---Intron-----FVLNEPQVYGRDKEKDEIVK
Sbul2:    AAERIKFHLAERTTERQVATRQTG---Intron-----FVLNEPQVYGRDKEKDEIVK

Sbul1:    ILINNVSNAQTL PVLPIILGMGGLGKTTLAQMVFNDRVIEHFHPKIWICVSEDFNEKRLI
Sbul2:    ILINIVSDAQTL S VLPILGMGGLGKTTLAQMVFNDRVIEHFLPKIWICVSEDFNEKRLI

Sbul1:    KEIVESIEEKS LGMDLAPLQKKLRDLLNGKKYLLVLDDVWNEDQDKWAKLRQVLKVGA
Sbul2:    KEIVESIEEKS LGMDLAPLQKKLQDLLNGKKYLLVLDDIWNEDQDKWAKLREVLKVGA

Sbul1:    SGASVLTTTRLEKVGSIMGTLPYELSNLSQEDCWLLFMQRAFGHQEEINLNLVAIGKEI
Sbul2:    SGASILTTTRLEKVGSIMQTLQPYELSNLCQEDCWLLFMQRAFGHQEEINHNLVAIGKEI

Sbul1:    VKKCGGVPLAAKTLGGILRFKREERQWEHV RDSEIWKL PQEESSILPALRLSYHHLPLDL
Sbul2:    VKKCGGVPLAAKTLGGILRFKROERQWEHV RDSEIWKL PQEESSILPALKLSYHHLPLDL

Sbul1:    RQCFTYCAVFPKDTMEKGNLISLWMAHGFI LSKGNLELENVGNEVWNELYLRSFFQEIE
Sbul2:    RQCF SYCAVFPKDTKMEKENLISLWMAHGFL LSKGNLELEDVGNEVWNELYLRSFFQEIE

Sbul1:    VKSGQTYFKMHDLIHDLATSLFSASTSSSNIREIIVENYIHMMSIGFTKVVSSYSLSHL
Sbul2:    VTYGKT YFKMHDLIHDLATSLFSASASSNNIREINVKGYPHMMSIGFAKVVSFYSRSHF

Sbul1:    QKFVSLRVLNLS DIKLQQLPSSIGDLVHLRYLNLSGNTSIRSLPNQLCKLQNLQTLDLHGC
Sbul2:    QKFVSLRVLNLSNLELKQLPSSIGDLVHLRYLNLSDN NRIRSLPKQLCKLQNLQTLDLRCC

Sbul1:    HSLCCLPKETSKLGSLRNLLLDGCGYGLTCMPPRIGSLTCLKTLSRFVVG IQKKSQLGELR
Sbul2:    YRLSCLPKETSKLGSLRNLLLD RCHGLTCMPPRIGSLTCLKTLD RFAMG-REKSPQIGELR

Sbul1:    NLNLYGSIETHLERVKNDMDAKEANLSAKENLHSLSMKWDDDERPRIYESEKVEVLE
Sbul2:    NLNLYGSI SITHLERVKNDMDAKEANLSSKENLHSLSMI WDEDERPHRYESEDVEVLE

Sbul1:    ALKPHSNLTCLTIRGFRGIRLPDWMNH SVLKNVVSIEIISCKNCSCLPFGELPCLKSLEL
Sbul2:    ALKPHSNLTCLTIIGFRGIRLPDWMNH SVLKNVVSLEISDCCKNCSCLPFGELPCLNSLQL

Sbul1:    WRGSAEVEYVDSGFPTRRRFP SLRKLNIREFDNLKGLLKKEGEEQCPVLEEIEIKC
Sbul2:    WSGSAEVEYIDSGFPTRRRFP SLRKLIIG EFDNLKGLVKKEGEEQFPVLEEMEINW

```

FIG. 6A

7/17

Sbul1: CPMFVIPTLSSVKKLVVSGDKSDAIGFSSISNLMALTSIQIRYNKEDASLPEEMFKSLANL
Sbul2: CPMFVIPTLSSVNKLVVSGEESDAIGFSSISNLRALTSLNISYNSEATSLPEEMFKSLANL

Sbul1: KYLNISFYFNLKELPTSLASLNALKHLEIHSCYALESLPPEGVKGLISLTQLSITYCEMLQ
Sbul2: KYLNIYYFKNLKELPTNLASLNALKNLEIESCYALESLPPEGVKGLTSLTQLSITYCTMLQ

Sbul1: CLPEGLQHLTALTNLSVEFCPTLAKRCEKGIGEDWYKIAHIPRVFIY*
Sbul2: CLPEGLQHLTALTNLSVRDCPTLAKRCEKGIGEDWYKIAHIPDVFIR*

FIG. 6B

8/17

Alignment of *Sbul1* (SEQ ID NO:3) and *Sbul2* (SEQ ID NO:5)
gene sequences

```

Sbul1  CCAACATCTTACTTCATTTCAAAAAATATAGATTCAATTGCGTACTCACAATACTCTATGGCTGAAGCTTTCCTTCAAGTT
                                             MetAlaGluAlaPheLeuGlnVal>
                                             EXON1
Sbul2  CCAACATCTTACTTCATTTCAAAAAATATAGATTCAATTGCTTcCTCACAATACTCTATGGCTGAAGCTTTCCTTCAAGTT>
Sbul1  CCAACATCTTACTTCATTTCAAAAAATATAGATTCAATTGCGTACTCACAATACTCTATGGCTGAAGCTTTCCTTCAAGTT

Sbul1  CTGTTAGACAATCTGACTTGTTTCATCCAAGGGGAACCTGGATTGATTCTTGGTTTTAAGGATGAGTTCGAAAAGCTTCA
LeuLeuAspAsnLeuThrCysPheIleGlnGlyGluLeuGlyLeuIleLeuGlyPheLysAspGluPheGluLysLeuGln>
                                             EXON1
Sbul2  CTGTTAGACAATCTGACTTGTTTCATCCAAGGGGAAGTGGATTGATTCTTGGTTTTAAGGATGAGTTCGAAAAGCTTCA>
Sbul1  CTGTTAGACAATCTGACTTGTTTCATCCAAGGGGAACCTGGATTGATTCTTGGTTTTAAGGATGAGTTCGAAAAGCTTCA

Sbul1  AAGCACGTTTACTACAATCCAAGCTGTGCTAGAAAGATGCTCAGAAGAAGCAATTGAAGGACAAGGCAATAGAAAATTGGT
SerThrPheThrThrIleGlnAlaValLeuGluAspAlaGlnLysLysGlnLeuLysAspLysAlaIleGluAsnTrp>
                                             EXON1
Sbul2  AAGCACATTTACTACAATCCAAGCTGTGCTAGAAAGATGCTCAGAAGAAGCAATTGAAGGACAAGGCAATAGAAAATTGGT>
Sbul1  AAGCACGTTTACTACAATCCAAGCTGTGCTAGAAAGATGCTCAGAAGAAGCAATTGAAGGACAAGGCAATAGAAAATTGGT

Sbul1  TGCAGAACTCAATGCTGCTGCATATGAGGCTGATGACATCTTGGACGAATGTAAACTGAGGCACCAATTAGACAGAAG
LeuGlnLysLeuAsnAlaAlaAlaTyrGluAlaAspAspIleLeuAspGluCysLysThrGluAlaProIleArgGlnLys>
                                             EXON1
Sbul2  TGCAGAACTCAATGCTGCTGTATATGAaGCTGAcGACATCTTGGACGAATGTAAACTGAGGCACCAATTAGACAGAAG>
Sbul1  TGCAGAACTCAATGCTGCTGCATATGAGGCTGATGACATCTTGGACGAATGTAAACTGAGGCACCAATTAGACAGAAG

Sbul1  AAGAACAAATATGGGTGTTATCATCCAAACGTTATCACTTTTCGTCACAAGATTGGGAAAAGGATGAAAAAGATTATGGA
LysAsnLysTyrGlyCysTyrHisProAsnValIleThrPheArgHisLysIleGlyLysArgMetLysLysIleMetGlu>
                                             EXON1
Sbul2  AAGAACAAATATGGGTGTTATCATCCAAACGTTATCgCTTTcCGTCACAAGATTGGGAAAAGGATGAAAAAGATTATGGA>
Sbul1  AAGAACAAATATGGGTGTTATCATCCAAACGTTATCACTTTTCGTCACAAGATTGGGAAAAGGATGAAAAAGATTATGGA

```

FIG. 7A

9/17

[illegible]

FIG. 7B

10/17

[illegible]

FIG. 7C

[illegible]

FIG. 7D

12/17

Sbul1 CAATGCTTTACATATTGTGCAGTATTCCCAAAGGATACCGAAATGGAAAAGGAAATCTAATCTCTCTCTGGATGGCCACA
GlnCysPheThrTyrCysAlaValPheProLysAspThrGluMetGluLysGlyAsnLeuIleSerLeuTrpMetAlaHis>
EXON2>

Sbul2 CAATGCTTTtCATATTGTGCAGTATTCCCAAAGGATACCGAAATGGAAAAGGAAATCTAATCTCTCTCTGGATGGCCACA>
|||||*|||||*|||||*|||||

Sbul1 CAATGCTTTACATATTGTGCAGTATTCCCAAAGGATACCGAAATGGAAAAGGAAATCTAATCTCTCTCTGGATGGCCACA

Sbul1 TGGTTTTATTTTATCGAAAGGAACTTGGAGCTAGAGAATGTAGGTAATGAAGTATGGAATGAATTATACTTGAGGTCTT
GlyPheIleLeuSerLysGlyAsnLeuGluLeuGluAsnValGlyAsnGluValTrpAsnGluLeuTyrLeuArgSer>
EXON2>

Sbul2 TGGTTTTtTTTTATCGAAAGGAACTTGGAGCTAGAGgATGTAGGTAATGAAGTATGGAATGAATTATACTTGAGGTCTT>
|||||*|||||*|||||*|||||

Sbul1 TGGTTTTATTTTATCGAAAGGAACTTGGAGCTAGAGAATGTAGGTAATGAAGTATGGAATGAATTATACTTGAGGTCTT

Sbul1 TCTTCCAAGAGATTGAAGTTAAATCTGGTCAAACCTTATTTCAAGATGCATGATCTCATTCTCATGATCTGGCAACATCTCTA
PhePheGlnGluIleGluValLysSerGlyGlnThrTyrPheLysMetHisAspLeuIleHisAspLeuAlaThrSerLeu>
EXON2>

Sbul2 TCTTCCAAGAGATTGAAGTTAcAtATGGTAAAACTTATTTCAAGATGCATGATCTCATcCATGATtTGGctACATCTCTA>
|||||*|||||*|||||*|||||*|||||*|||||*|||||

Sbul1 TCTTCCAAGAGATTGAAGTTAAATCTGGTCAAACCTTATTTCAAGATGCATGATCTCATTCTCATGATCTGGCAACATCTCTA

Sbul1 TTTTCGGCAAGCACATCAAGCAGCAATATCCGAGAAATAATGTAGAAAATTACATACATATGATGTCATTGGTTTCAC
PheSerAlaSerThrSerSerSerAsnIleArgGluIleIleValGluAsnTyrIleHisMetMetSerIleGlyPheThr>
EXON2>

Sbul2 TTTTCGGCAAGCgCATCAAGCAaCAATATCCGtGAAATAaATGTAAaggTTACccACATATGATGTCgATTGGcTtgC>
|||||*|||||*|||||*|||||*|||||*||**||**|||*|||||*||**

Sbul1 TTTTCGGCAAGCACATCAAGCAGCAATATCCGAGAAATAATGTAGAAAATTACATACATATGATGTCCATTGGTTTCAC

Sbul1 TAAAGTGGTATCTTCTTACTCTCTTTCCCACTTGCAGAAAGTTGTCTCGTTGAGGGTGCTTAATCTAAGTGACATAAAAC
LysValValSerSerTyrSerLeuSerHisLeuGlnLysPheValSerLeuArgValLeuAsnLeuSerAspIleLys>
EXON2>

Sbul2 aAAAGTGGTgTCTTtTtACTCTCgTtCTCACTTcCAaAAGTTTGTCTCGTtaAGGGTGCTTAATCTAAGTaActTAgAAC>
||||||||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||

Sbul1 TAAAGTGGTATCTTCTTACTCTCTTTCCCACTTGCAGAAAGTTGTCTCGTTGAGGGTGCTTAATCTAAGTGACATAAAAC

FIG. 7E

Sbul1 TTAAGCAGTTACCGTCTTCcATTGGAGATCTAGTAcATTAAAGATACCTAAAacTTGTCTGGCAATActAGtATTcGTagT
LeuLysGlnLeuProSerSerIleGlyAspLeuValHisLeuArgTyrLeuAsnLeuSerGlyAsnThrSerIleArgSer>
EXON2>

Sbul2 TcAAGCAGTTACCAtCTTCaATTGGgGATCTAGTACATTAAAGATACCTAAACTTGtCTGaCaATAaTAGaATTcGTagT>
|*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||>

Sbul1 TTAAGCAGTTACCGTCTTCcATTGGAGATCTAGTACATTAAAGATACCTAAACTTGtCTGGCAATActAGtATTcGTagT

Sbul1 CTCCAAACCAGTTATGCAGCTTCAAATCTGCAGACTCTTGATCTACatGGCTGtCATTCActTTGTTGTTGCCAAa
LeuProAsnGlnLeuCysLysLeuGlnAsnLeuGlnThrLeuAspLeuHisGlyCysHisSerLeuCysCysLeuProLys>
EXON2>

Sbul2 CTTCCcAagCAGTTATGCAGCTTCAAATCTGCAGACTCTTGATCTACgTtGtTGctAcagACTTTcTGTttGCCAAa>
||||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||>

Sbul1 CTTCCAAACCAGTTATGCAGCTTCAAATCTGCAGACTCTTGATCTACatGGCTGtCATTCActTTGTTGTTGCCAAa

Sbul1 AGAAACAAGCAAactTGGTAGTCTTCGAATCTTTACTTGATGGTTGCTATGGATTGACTTGTATGCCACCAAGGATAg
GluThrSerLysLeuGlySerLeuArgAsnLeuLeuLeuAspGlyCysTyrGlyLeuThrCysMetProProArgIle>
EXON2>

Sbul2 AGAAACAAGCAAactTGGTAGTCTcCGAAATCTTTACTTGATcGTTGccATGGATTGACTTGTATGCCACCAAGGATAg>
|||||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||>

Sbul1 AGAAACAAGCAAactTGGTAGTCTTCGAATCTTTACTTGATGGTTGCTATGGATTGACTTGTATGCCACCAAGGATAg

Sbul1 GATCTTTGACATGCCTTAAGACTCTAAGTAGATTGTGGTGGGAATTAGAAGAAAGTTGTCAACTTGGTGAATTACGA
GlySerLeuThrCysLeuLysThrLeuSerArgPheValValGlyIleGlnLysLysSerCysGlnLeuGlyGluLeuArg>
EXON2>

Sbul2 GATCATTGACATGCCTTAAGACTCTAGATCGCTTTGCAATGGGAA---GGGAGAAAGTCCTCAAATTGGTGAATTACGA
|||*|||*|||*|||*|||**|||*|||***|||****|||*|||*|||*|||*|||*|||*|||>

Sbul1 GATCTTTGACATGCCTTAAGACTCTAAGTAGATTGTGGTGGGAATTAGAAGAAAGTTGTCAACTTGGTGAATTACGA

Sbul1 AACCTGAATCTCTATGGCTCAATTGAAATCACGCATCTTGAGAGAGTGAAGAATGATATGGATGCAAAAGAAGCCAATTT
AsnLeuAsnLeuTyrGlySerIleGluIleThrHisLeuGluArgValLysAsnAspMetAspAlaLysGluAlaAsnLeu>
EXON2>

Sbul2 AACCTGAATCTCTATGGCTCAATTtcAATCACGCATCTTGAGAGAGTGAAGAATGATATGGATGCAAAAGAAGCCAATTT>
|||||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||>

Sbul1 AACCTGAATCTCTATGGCTCAATTGAAATCACGCATCTTGAGAGAGTGAAGAATGATATGGATGCAAAAGAAGCCAATTT

FIG. 7F

[illegible]

FIG. 7G

[illegible]

FIG. 7H

[illegible]

FIG. 7I

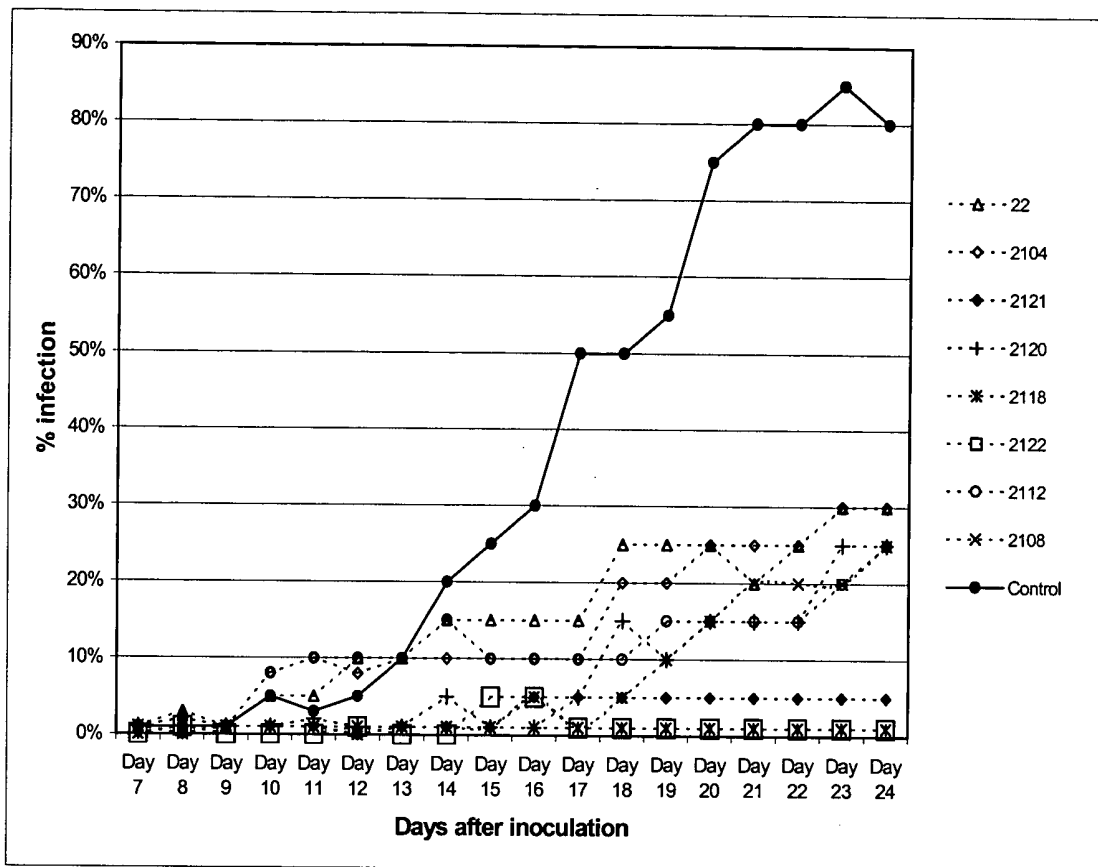


FIG. 8